

DETECTION AND QUANTIFICATION OF MODIFIED PROTEINS

Abstract

The invention provides a method detecting and quantifying proteins by mass spectrophotometric analysis using peptide internal standards and provides a highly sensitive way of detecting protein modifications. In one aspect, the invention provides a method for determining a site of ubiquitination in a polypeptide and for evaluating ubiquitination targets in a population of polypeptides. In this way, a proteome ubiquitination map can be obtained which comprises information relating to the ubiquitination states of a plurality of cellular polypeptides. Maps can be obtained for a variety of different types of cells and cell states. For example, ubiquitination targets in normal and diseased cells can be evaluated. Preferably, the map is stored as data files in a database. Individual ubiquitinated polypeptides identified can be used to generate molecular probes diagnostic of a cell state and/or can serve as targets for agents that modulate one or more cellular processes.

BOS2_328121.1